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Respectfully submitted,



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I hereby certify that this correspondence is being
deposited with the United States Postal service as first
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on September 27, 2001
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Appendix A Marked up Version

On page 21, starting on line 16 and ending on 21:

In this library, the expected highest peaks are those representing His in the final amino acid position (X_2 -His-Pro-Gln-Phe-Ala-Ala-Ala-thread (SEQ ID NO:1)). The endcapping species should make less difference (Devlin et al., *Science* **1990**, *249*, 404-406; Lam et al., *Nature* **1991**, *354*, 82-82; Schmidt et al., *J. Mol. Biol.* **1996**, *255*, 753-766). Both of these expected results are seen. Profiles for group fitness at a given position may be obtained by cyclic averaging over appropriate shorter cycle times that correspond to a given cylinder.

On page 22, starting on line 26 and ending on line 36:

A small library of 35 peptides was prepared, as (X_2 - X_1 -Pro-Gln-Phe-Ala-Ala-Ala-thread (SEQ ID NO:2)). H-Pro-Gln-Phe-Ala-Ala-Ala-thread (SEQ ID NO:2) was prepared by couplings to the whole thread in a flask; only the X_1 and X_2 amino acids which constitute the library variation were added while the thread was wrapped around a cylinder. The thread was wrapped around the 5 cm circumference cylinder to couple X_1 , which is chosen from (FMOC) His, Ser, Asp, Ala, Phe (denoted A-E respectively). After endcapping, deprotection, and wrapping around the 7 cm cylinder, X_2 , chosen from Leu, Boc-Phe, Bz, Ac, His, Glu, Gly (denoted 1-7 respectively) was added. The Boc-Phe results in a free amine terminus, while the other amino acids, coupled as their FMOC derivatives, are N acetylated before binding studies. Fmoc deprotection and acetylation were followed by deprotection of sidechains in 50% TFA / DCM for 2 h. The library was rinsed thoroughly, blocked by incubation with 3% bovine serum albumin, and exposed to streptavidin-fluorescein conjugate. The thread was dried, and then read on the thread reader.

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On page 27, starting on line 1 and ending on line 3:



In this library, the expected highest peaks are those representing His in the final amino acid position (X_2 -His-Pro-Gln-Phe-Ala-Ala-Ala-thread (SEQ ID NO:3)). The endcapping species should make less difference. Both of these expected results are seen.